

P. TUNG

#5
5/30/00 B

PAGE: 1

RAW SEQUENCE LISTING
PATENT APPLICATION US/09/318,528DATE: 05/26/2000
TIME: 11:48:05

Input Set: I318528.RAW

<p>This Raw Listing contains the General Information Section and up to first 5 pages.</p>

ENTERED

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1  <110> APPLICANT: Kretz, Keith
2  <120> TITLE OF INVENTION: NOVEL PHYTASE
3  <130> FILE REFERENCE: 09010/029003
4  <140> CURRENT APPLICATION NUMBER: US/09/318,528
5  <141> CURRENT FILING DATE: 1999-05-25
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7  <151> EARLIER FILING DATE: 1999-04-13
8  <150> EARLIER APPLICATION NUMBER: 08/910,798
9  <151> EARLIER FILING DATE: 1997-08-13
10 <150> EARLIER APPLICATION NUMBER: 09/259,214
11 <151> EARLIER FILING DATE: 1999-03-01
12 <160> NUMBER OF SEQ ID NOS: 4
13 <170> SOFTWARE: FastSEQ for Windows Version 4.0
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15 <211> LENGTH: 1323
16 <212> TYPE: DNA
17 <213> ORGANISM: Escherichia coli
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19 <221> NAME/KEY: CDS
20 <222> LOCATION: (1)...(1320)
21 <221> NAME/KEY: misc_feature
22 <222> LOCATION: (1)...(1323)
23 <223> OTHER INFORMATION: n = A,T,C or G
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26     Met Lys Ala Ile Leu Ile Pro Phe Leu Ser Leu Leu Ile Pro Leu Thr
27         1             5             10             15
28     ccg caa tct gca ttc gct cag agt gag ccg gag ctg aag ctg gaa agt      96
29     Pro Gln Ser Ala Phe Ala Gln Ser Glu Pro Glu Leu Lys Leu Glu Ser
30         20             25             30
31     gtg gtg att gtc agt cgt cat ggt gtg cgt gct cca acc aag gcc acg      144
32     Val Val Ile Val Ser Arg His Gly Val Arg Ala Pro Thr Lys Ala Thr
33         35             40             45
34     caa ctg atg cag gat gtc acc cca gac gca tgg cca acc tgg ccg gta      192
35     Gln Leu Met Gln Asp Val Thr Pro Asp Ala Trp Pro Thr Trp Pro Val
36         50             55             60
W--> 37     aaa ctg ggt tgg ctg aca ccg cgn ggt ggt gag cta atc gcc tat ctc      240
38     Lys Leu Gly Trp Leu Thr Pro Arg Gly Gly Glu Leu Ile Ala Tyr Leu
39         65             70             75             80
40     gga cat tac caa cgc cag cgt ctg gta gcc gac gga ttg ctg gcg aaa      288
41     Gly His Tyr Gln Arg Gln Arg Leu Val Ala Asp Gly Leu Leu Ala Lys
42         85             90             95
43     aag ggc tgc ccg cag tct ggt cag gtc gcg att att gct gat gtc gac      336
44     Lys Gly Cys Pro Gln Ser Gly Gln Val Ala Ile Ile Ala Asp Val Asp

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45		100		105		110		
46	gag	cgt	acc	cgt	aaa	aca	ggc	gaa gcc ttc gcc gcc ggg ctg gca cct 384
47	Glu	Arg	Thr	Arg	Lys	Thr	Gly	Glu Ala Phe Ala Ala Gly Leu Ala Pro
48		115		120		125		
49	gac	tgt	gca	ata	acc	gta	cat	acc cag gca gat acg tcc agt ccc gat 432
50	Asp	Cys	Ala	Ile	Thr	Val	His	Thr Gln Ala Asp Thr Ser Ser Pro Asp
51		130		135		140		
52	ccg	tta	ttt	aat	cct	cta	aaa	act ggc gtt tgc caa ctg gat aac gcg 480
53	Pro	Leu	Phe	Asn	Pro	Leu	Lys	Thr Gly Val Cys Gln Leu Asp Asn Ala
54		145		150		155		160
55	aac	gtg	act	gac	gcg	atc	ctc	agc agg gca gga ggg tca att gct gac 528
56	Asn	Val	Thr	Asp	Ala	Ile	Leu	Ser Arg Ala Gly Gly Ser Ile Ala Asp
57		165		170		175		
58	ttt	acc	ggg	cat	cgg	caa	acg	gcg ttt cgc gaa ctg gaa cgg gtg ctt 576
59	Phe	Thr	Gly	His	Arg	Gln	Thr	Ala Phe Arg Glu Leu Glu Arg Val Leu
60		180		185		190		
61	aat	ttt	ccg	caa	tca	aac	ttg	tgc ctt aaa cgt gag aaa cag gac gaa 624
62	Asn	Phe	Pro	Gln	Ser	Asn	Leu	Cys Leu Lys Arg Glu Lys Gln Asp Glu
63		195		200		205		
64	agc	tgt	tca	tta	acg	cag	gca	tta cca tcg gaa ctc aag gtg agc gcc 672
65	Ser	Cys	Ser	Leu	Thr	Gln	Ala	Leu Pro Ser Glu Leu Lys Val Ser Ala
66		210		215		220		
67	gac	aat	gtc	tca	tta	acc	ggt	gcg gta agc ctc gca tca atg ctg acg 720
68	Asp	Asn	Val	Ser	Leu	Thr	Gly	Ala Val Ser Leu Ala Ser Met Leu Thr
69		225		230		235		240
70	gag	ata	ttt	ctc	ctg	caa	caa	gca cag gga atg ccg gag ccg ggg tgg 768
71	Glu	Ile	Phe	Leu	Leu	Gln	Gln	Ala Gln Gly Met Pro Glu Pro Gly Trp
72		245		250		255		
73	gga	agg	atc	acc	gat	tca	cac	cag tgg aac acc ttg cta agt ttg cat 816
74	Gly	Arg	Ile	Thr	Asp	Ser	His	Gln Trp Asn Thr Leu Leu Ser Leu His
75		260		265		270		
76	aac	gcg	caa	ttt	tat	ttg	cta	caa cgc acg cca gag gtt gcc cgc agc 864
77	Asn	Ala	Gln	Phe	Tyr	Leu	Leu	Gln Arg Thr Pro Glu Val Ala Arg Ser
78		275		280		285		
79	cgc	gcc	acc	ccg	tta	ttg	gat	ttg atc atg gca gcg ttg acg ccc cat 912
80	Arg	Ala	Thr	Pro	Leu	Leu	Asp	Leu Ile Met Ala Ala Leu Thr Pro His
81		290		295		300		
82	cca	ccg	caa	aaa	cag	gcg	tat	ggt gtg aca tta ccc act tca gta ctg 960
83	Pro	Pro	Gln	Lys	Gln	Ala	Tyr	Gly Val Thr Leu Pro Thr Ser Val Leu
84		305		310		315		320
85	ttt	att	gcc	gga	cac	gat	act	aat ctg gca aat ctc ggc ggc gca ctg 1008
86	Phe	Ile	Ala	Gly	His	Asp	Thr	Asn Leu Ala Asn Leu Gly Gly Ala Leu
87		325		330		335		
88	gag	ctc	aac	tgg	acg	ctt	ccc	ggt cag ccg gat aac acg ccg cca ggt 1056
89	Glu	Leu	Asn	Trp	Thr	Leu	Pro	Gly Gln Pro Asp Asn Thr Pro Pro Gly
90		340		345		350		
91	ggt	gaa	ctg	gtg	ttt	gaa	cgc	tgg cgt cgg cta agc gat aac agc cag 1104
92	Gly	Glu	Leu	Val	Phe	Glu	Arg	Trp Arg Arg Leu Ser Asp Asn Ser Gln
93		355		360		365		
94	tgg	att	cag	gtt	tcg	ctg	gtc	ttc cag act tta cag cag atg cgt gat 1152

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95      Trp Ile Gln Val Ser Leu Val Phe Gln Thr Leu Gln Gln Met Arg Asp
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97      aaa acg ccg ctg tca tta aat acg ccg ccc gga gag gtg aaa ctg acc      1200
98      Lys Thr Pro Leu Ser Leu Asn Thr Pro Pro Gly Glu Val Lys Leu Thr
99          385                      390                      395                      400
100     ctg gca gga tgt gaa gag cga aat gcg cag ggc atg tgt tcg ttg gca      1248
101     Leu Ala Gly Cys Glu Glu Arg Asn Ala Gln Gly Met Cys Ser Leu Ala
102                      405                      410                      415
103     ggt ttt acg caa atc gtg aat gaa gca cgc ata ccg gcg tgc agt ttg      1296
104     Gly Phe Thr Gln Ile Val Asn Glu Ala Arg Ile Pro Ala Cys Ser Leu
105                      420                      425                      430
106     aga tct cat cac cat cac cat cac taa      1323
107     Arg Ser His His His His His His
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111     <212> TYPE: PRT
112     <213> ORGANISM: Escherichia coli
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116     Pro Gln Ser Ala Phe Ala Gln Ser Glu Pro Glu Leu Lys Leu Glu Ser
117          20                      25                      30
118     Val Val Ile Val Ser Arg His Gly Val Arg Ala Pro Thr Lys Ala Thr
119          35                      40                      45
120     Gln Leu Met Gln Asp Val Thr Pro Asp Ala Trp Pro Thr Trp Pro Val
121          50                      55                      60
122     Lys Leu Gly Trp Leu Thr Pro Arg Gly Gly Glu Leu Ile Ala Tyr Leu
123          65                      70                      75                      80
124     Gly His Tyr Gln Arg Gln Arg Leu Val Ala Asp Gly Leu Leu Ala Lys
125          85                      90                      95
126     Lys Gly Cys Pro Gln Ser Gly Gln Val Ala Ile Ile Ala Asp Val Asp
127          100                     105                     110
128     Glu Arg Thr Arg Lys Thr Gly Glu Ala Phe Ala Ala Gly Leu Ala Pro
129          115                     120                     125
130     Asp Cys Ala Ile Thr Val His Thr Gln Ala Asp Thr Ser Ser Pro Asp
131          130                     135                     140
132     Pro Leu Phe Asn Pro Leu Lys Thr Gly Val Cys Gln Leu Asp Asn Ala
133          145                     150                     155                     160
134     Asn Val Thr Asp Ala Ile Leu Ser Arg Ala Gly Gly Ser Ile Ala Asp
135          165                     170                     175
136     Phe Thr Gly His Arg Gln Thr Ala Phe Arg Glu Leu Glu Arg Val Leu
137          180                     185                     190
138     Asn Phe Pro Gln Ser Asn Leu Cys Leu Lys Arg Glu Lys Gln Asp Glu
139          195                     200                     205
140     Ser Cys Ser Leu Thr Gln Ala Leu Pro Ser Glu Leu Lys Val Ser Ala
141          210                     215                     220
142     Asp Asn Val Ser Leu Thr Gly Ala Val Ser Leu Ala Ser Met Leu Thr
143          225                     230                     235                     240
144     Glu Ile Phe Leu Leu Gln Gln Ala Gln Gly Met Pro Glu Pro Gly Trp

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145		245		250		255
146	Gly Arg Ile Thr Asp Ser His Gln Trp Asn Thr Leu Leu Ser Leu His					
147		260		265		270
148	Asn Ala Gln Phe Tyr Leu Leu Gln Arg Thr Pro Glu Val Ala Arg Ser					
149		275		280		285
150	Arg Ala Thr Pro Leu Leu Asp Leu Ile Met Ala Ala Leu Thr Pro His					
151		290		295		300
152	Pro Pro Gln Lys Gln Ala Tyr Gly Val Thr Leu Pro Thr Ser Val Leu					
153		305		310		315
154	Phe Ile Ala Gly His Asp Thr Asn Leu Ala Asn Leu Gly Gly Ala Leu					
155		325		330		335
156	Glu Leu Asn Trp Thr Leu Pro Gly Gln Pro Asp Asn Thr Pro Pro Gly					
157		340		345		350
158	Gly Glu Leu Val Phe Glu Arg Trp Arg Arg Leu Ser Asp Asn Ser Gln					
159		355		360		365
160	Trp Ile Gln Val Ser Leu Val Phe Gln Thr Leu Gln Gln Met Arg Asp					
161		370		375		380
162	Lys Thr Pro Leu Ser Leu Asn Thr Pro Pro Gly Glu Val Lys Leu Thr					
163		385		390		395
164	Leu Ala Gly Cys Glu Glu Arg Asn Ala Gln Gly Met Cys Ser Leu Ala					
165		405		410		415
166	Gly Phe Thr Gln Ile Val Asn Glu Ala Arg Ile Pro Ala Cys Ser Leu					
167		420		425		430
168	Arg Ser His His His His His His					
169		435		440		

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170 <210> SEQ ID NO 3
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172 <212> TYPE: DNA
173 <213> ORGANISM: Artificial Sequence
174 <220> FEATURE:
175 <223> OTHER INFORMATION: Oligonucleotide
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178 <210> SEQ ID NO 4
179 <211> LENGTH: 33
180 <212> TYPE: DNA
181 <213> ORGANISM: Artificial Sequence
182 <220> FEATURE:
183 <223> OTHER INFORMATION: Oligonucleotide
184 <400> SEQUENCE: 4
185      gtttctggat ccttacaaac tgcacgccgg tat

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49

33

Input Set: I318528.RAW

Line	Error/Warning	Original Text
37	W "N" or "Xaa" used: Feature required	aaa ctg ggt tgg ctg aca ccg cgn ggt ggt g